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Amendments to the Specification

Please replace paragraph 1 on page 17 with the following amended paragraph:

Peptides produced by expression of the polynucleotides of the present invention can be obtained by transforming a host cell by any of the previously described methods, growing the host cell under appropriate conditions, inducing expression of the polynucleotide and isolating the protein(s) of interest. If the protein ~~in~~ **is** retained within the host cell, the protein can be obtained by lysis of the host cells, while if the protein is a secreted protein, it can be isolated from the culture medium. Several methods are available for purification of proteins and are known to those of ordinary skill in the art. These include precipitation by, for example, ammonium sulfate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, affinity chromatography, hydroxylapatite chromatography, lectin chromatography, high performance liquid chromatography (HPLC), electrophoresis under native or denaturing conditions, isoelectric focusing, and immunoprecipitation.

Please replace paragraph 1 on page 18 with the following amended paragraph:

For solid-phase peptide synthesis, the procedure entails the sequential assembly of the appropriate amino acids into a peptide of a desired sequence while the end of the growing peptide is linked to an insoluble support. Usually, the carboxyl terminus of the peptide is linked to a polymer from which it can be liberated upon treatment with a cleavage reagent. In a common method, an amino acid is bound to a resin particle, and the peptide generated in a stepwise manner by successive additions of protected amino acids to produce a chain of amino acids. Modifications of the technique described by Merrifield are commonly used (see, e.g., Merrifield, *J. Am. Chem. Soc.* 96: 2989-93, 1964). In an automated solid-phase method, peptides are synthesized by loading the carboxy-terminal amino acid onto an organic linker (e.g., PAM, 4-oxymethylphenylacetamidomethyl), which is covalently attached to an insoluble polystyrene resin cross-linked with divinyl benzene. The terminal amine may be

protected by blocking with t-butyloxycarbonyl. Hydroxyl- and carboxyl-groups are commonly protected by blocking with O-benzyl groups. Synthesis is accomplished in an automated peptide synthesizer, a number of which are commercially available. Following synthesis, the product may be removed from the resin. The blocking groups are removed typically by using hydrofluoric acid or trifluoromethyl sulfonic acid according to established methods (e.g., Bergot and McCurdy, *Applied Biosystems Bulletin*, 1987). Following cleavage and purification, a yield of approximately 60 to 70% is typically produced. Purification of the product peptides is accomplished by, for example, crystallizing the peptide from an organic solvent such as methyl-butyl ether, then dissolving in distilled water, and using dialysis (if the molecular weight of the subject peptide is greater than about 500 daltons) or reverse high-pressure liquid chromatography (e.g., using a ~~C.sup.18~~ C^{18} column with 0.1% trifluoroacetic acid and acetonitrile as solvents) if the molecular weight of the peptide is less than 500 daltons. Purified peptide may be lyophilized and stored in a dry state until use. Analysis of the resulting peptides may be accomplished using the common methods of analytical high pressure liquid chromatography (HPLC) and electrospray mass spectrometry (ES-MS).

Please replace paragraph 1 on page 23 with the following amended paragraph:

DNA sequences were translated using the "translate" program of the ExPASy Molecular Biology Server ~~(website http://www.expasy.ch/).~~ . Sequences were compared with nucleic acid and protein sequences stored in sequence databases (GenBank, EMBL, dbEST, SwissProt, PIR) using standard algorithms (i.e.) FASTA (Lipman and Person, *Science*, 227:1435-1441, 1985) and BLAST (Altschul et al., *J. Molecular Biol.*, 215:403-410, 1990) commands. Peptide sequences were aligned using ClustalW (Thompson et al., *Nuc. Acid Res.*, 22:4673-4680, 1994) with a PAM250 weight table and the dendogram viewed using TreeView (Page, *Computer Applic. Biosci.*, 12:357-358, 1996). The f8-mer DNA sequences obtained coded for 19 predicted peptide sequences (Table 1). The majority of the peptides contained amino acid residues that were predicted to be strong α-helical formers (i.e. Glu, Ala and Leu) and α-helical breakers (i.e. Gly and Pro). Despite the lack of a common motif, the

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ClustalW multiple sequence alignment program was used to cluster similar peptides in the form of a dendogram. The dendogram, constructed from the aligned peptides, indicated that the f8-mer peptide sequences could be grouped into six broad family groups as depicted in Figure 1 and Table 1. Selected sequences from the f88-4/15 mer library are shown in Table 2.

Please replace the Abstract on page 32 with the following:

A method for the identification of peptides having an affinity ~~for the surface of~~ fungi is provided as is a method for the identification of peptides capable of affecting the development of a fungus. Also provided are compositions ~~**comprising**~~ **containing** peptides identified using the method of the present invention. In addition, isolated polynucleotides, vectors, expression cassettes and transformed cells capable of expressing peptides identified by the method of the present invention are provided.